means for measuring peak intensity and size of each DNA fragment in a sample of genomic DNA;

means for classifying the peak intensities of said fragments according to a predetermined discrete intensity level scale;

means for aligning the sizes of said fragments into corresponding ones of discrete size bins;

means for determining a sequence of fragments according to values of said bins;

means for entering the classified peak intensities of said fragments into a data record in said sequence; and

means storing the record in a computer-readable storage medium.–.

REMARKS

Claims 1-17 remain pending in this application. Reconsideration of this application is requested.

The rejection of claims 1-17 under the second paragraph of 35 U.S.C. § 112, and the objection to claims 2-5 as containing abbreviations, are respectfully traversed. It is axiomatic that claims, whether under examination or patented, must be read not in a vacuum, but in light of the specification. Each of the objected-to phrases in claims 8 and 15; 9, 16 and 17; and 11, is fully defined in the specification, such that its meaning is clear and unambiguous. Similarly, the abbreviations contained in claims 2-5 are defined in the specification. As such, there is nothing improper about abbreviations in a claim.

For example, claim 8 recites the step of "assigning a potential energy value to each cluster, said potential energy value being proportional to the spacing between adjacent peaks of the cluster and to the amount of displacement required to bin the peaks into discrete size bins." This step is disclosed in the specification at page 12, line 28, to page 13, line 16, and illustrated in Fig. 4 at step 1102. In particular, the potential energy value E is proportional to the displacement x_r of the peaks from the discrete size bins (see Figs. 3A-3B), and the displacement x_s between adjacent peaks of the cluster, by proportionality constants k_r and k_s respectively. Claims 8 and 15 are thus clear and

unambiguous on their face, and accurately reflect the disclosed invention. Those skilled in the art reading the specification would understand the scope and meaning of claims 8 and 15 without any confusion.

Similarly, the starting and ending sizes of fragments as set forth in claims 9 and 17, and the step of matching a data record to itself as set forth in claim 11, are fully and adequately disclosed in the specification, such that their meaning as used in the claims is definite, clear and unambiguous.

Similarly, claims 1 and 12 set forth that classified peak intensities of fragments are entered into a data record in a sequence determined by aligned sizes into corresponding discrete size bins. This step is fully disclosed in the specification and its meaning would be clear to anyone skilled in the art from the specification. However, claims 1 and 12 have been amended to clearly indicate that a sequence is determined by the aligned sizes.

The indefiniteness rejections appear to arise as a result of the Examiner's reading of the claims in a vacuum, divorced from the specification. This is not the proper manner in which claims are to be construed, either for purposes of examination or for purposes of infringement analysis. Consequently, the indefiniteness rejections are respectfully submitted to be improperly based, and should be withdrawn.

The rejection of claims 1, 2 and 5-17 under 35 U.S.C. § 103 as being unpatentable over Ghosh et al. in view of McEvoy et al., and the rejection of claims 1-17 under § 103 as being unpatentable over Ghosh et al. in view of McEvoy et al. and Young et al., are respectfully traversed.

The present invention as claimed is directed to a novel method and product for obtaining DNA fingerprint profile data. According to the invention, raw marker fragment peak intensity data is classified into discrete intensity levels according to a predetermined scale, as shown in Fig. 2. The sizes of the fragments are then aligned into corresponding discrete size bins, as shown in Fig. 3B. The processed data is then entered into a data record in a sequence of peak intensities determined by the aligned sizes in the bins, as shown in Fig. 5 (sequence 509).

Contrary to the invention as set forth in claims, neither Ghosh, nor McEvoy nor Young either 1) classify peak intensities of DNA fragments according to a predetermined discrete intensity level scale, 2) align fragment sizes into discrete size bins, and 3) enter the peak intensity data into a record in a sequence determined by the aligned sizes of the bins.

Ghosh discloses methods of sizing of alleles across multiple gels, as shown in Figs. 2 and 3, both for intergel variation and for variations across sequencers. Ghosh does not classify peak intensities into discrete intensity levels according to a predetermined scale, nor does Ghosh align the sizes of fragments into discrete size bins. Instead, Ghosh sorts alleles according to size, starting with a minimum allowable distance between adjacent bins, such as 0.4 bp (page 169, col. 2). When the size difference between two sequentially sized alleles is greater than the starting tolerance level, a new bin is created. Thus, as shown in Figs. 2 and 3, there are no discrete size bins into which fragments are aligned. Rather, as different sizes of alleles are found, additional bins are created.

McEvoy similarly relates simply to allele size calling techniques applicable across gels. McEvoy fails to disclose any method for obtaining DNA fingerprint profile data records as disclosed and claimed in the present application.

Young, cited by the Examiner for its disclosure of different methods for obtaining the DNA markers, is irrelevant to the present application, since the present application does not claim to have invented a method of obtaining the DNA markers per se. Young adds nothing to Ghosh or McEvoy which would cure the fundamental deficiencies of those references with respect to the claimed invention.

In summary, none of the prior art references of record discloses or suggests the novel method and product of the present application as set forth in the claims, whether considered individually or in any combination thereof. Favorable reconsideration of this application and the issuance of a Notice of Allowance are earnestly solicited.

Please charge any fee or credit any overpayment pursuant to 37 CFR 1.16 or 1.17 to Deposit Account No. 02-2135.

RESPECTFULLY SUBMITTED,			
NAME AND REG. NUMBER	Vincent M. DeLuca Attorney for Applicants Registration No. 32,408		
SIGNATURE	Vincent M DeLuca	DATE	10 DEC 02

Address	Rothwell, Figg, Ernst & Manbeck 1425 K Street, N.W., Suite 800				
City	Washington	*State*	D.C.	*Zip Code*	20005
Country	U.S.A.	*Telephone*	202-783-6040	*Fax*	202-783-6031

Attachments: Marked-Up Copies of Amendments

MARKED-UP COPY OF AMENDMENTS SHOWING CHANGES MADE

In the Claims:

1. (Amended) A method for obtaining DNA fingerprint profile data, comprising the steps of:

measuring peak intensity and size of each DNA fragment in a sample of genomic DNA;

classifying the peak intensities of said fragments according to a predetermined discrete intensity level scale;

aligning the sizes of said fragments into corresponding ones of discrete size bins;

determining a sequence of fragments according to values of said bins;

entering the classified peak intensities of said fragments into a data record in **[a] said** sequence **[**determined by said aligned sizes**]**; and

storing the record.

12. (Amended) A computer program product, comprising:

a computer-readable medium having computer-executable code recorded thereon for obtaining DNA fingerprint profile data, said computer-executable code comprising:

means for measuring peak intensity and size of each DNA fragment in a sample of genomic DNA;

means for classifying the peak intensities of said fragments according to a predetermined discrete intensity level scale;

means for aligning the sizes of said fragments into corresponding ones of discrete size bins;

means for determining a sequence of fragments according to values of said bins;

means for entering the classified peak intensities of said fragments into a data record in **[a] said** sequence **[**determined by said aligned sizes**]**; and

means storing the record in a computer-readable storage medium.